
--Predicted external domains of ABC1

TM1-TM2 (SEQ ID NO:3): 663 KEARLKETMRIMGLDNSI 680

TM3-TM4 (SEQ ID NO:4): 740 FSRAN 744

TM5-TM6 (SEQ ID NO:5): 795 ALFEEQGIGVQWDNLFESPVEEDGFN 820

TM7-TM8 1371

(SEQ ID NO:6):

FGKYPSLELQPWMYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTR
CMEGNPIPDTPCQAGEEEWTTAPVPQTIMDLFQNGNWTMQNPSACQ
CSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDLTGRNISDYL VKT
YVQIIAKSLKNKIWVNEFRYGGFSLGVSNTQALPPSQEVNDAIKQMKK
HLKLAKDSSADRFNLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLN
VINNAILRANLQKGENPSHYGITAFNHPLNLTKQQLSEVALMTTSVD
1654

TM9-TM10 (SEQ ID NO:7): 1741 LLLLYGWSITPLMYPASFVFKIP 1763

TH11-TH12 (SEQ ID NO:8): 1823 VKNQAMADALERFGENRFVSPLSW

DLVGR 1851--

Please replace the paragraph starting with "As also shown in Fig. 1" (lines 15-25) on page 26 of the application with the following paragraph:

--As also shown in Fig. 1, RFLP analysis confirmed the presence of the WHAM mutation in genomic DNA. Genomic DNA from normal and mutant homozygous male and hemizygous female chickens was amplified using PCR primers

forward:

5'-GTCACTTCCCAAACAAAGCTA-3'

SEQ ID No:9

reverse:

5'-ATGGACGCATTGAAGTTTCC-3'

SEQ ID No:10

flanking the WHAM mutation, then the PCR products digested with *Hinf*I.

The WHAM alteration destroys a *Hinf*I site, resulting in a 142 bp uncut fragment rather than the 106 bp and 36 bp fragments of normal chickens.

The chicken sex chromosomes of each bird tested are indicated below the photo; male chickens are ZZ, female chickens are ZW.--

In the drawings:

Per 37 C.F.R. 1.121(d), the applicants submit the enclosed Fig. 1 with the proposed changes shown in red for approval by the Examiner.